OIPE

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RAW SEQUENCE LISTING　　　　　　　DATE: 01/16/2003
PATENT APPLICATION:　**US/09/975,723A**　　TIME: 14:19:52

Input Set : **A:\601-1-101N SEQUENCE LISTING.TXT**
Output Set: **N:\CRF4\01162003\I975723A.raw**

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 4 <110> APPLICANT: Nackman, Gary
 5         Foty, Ramsey
 7 <120> TITLE OF INVENTION: Improvement of Endothelial Cell-Cell
 8         Cohesion
10 <130> FILE REFERENCE: 601-1-101N
12 <140> CURRENT APPLICATION NUMBER: 09/975,723A
13 <141> CURRENT FILING DATE: 2001-10-11
15 <150> PRIOR APPLICATION NUMBER: 60/241,216
16 <151> PRIOR FILING DATE: 2000-10-13
18 <150> PRIOR APPLICATION NUMBER: 60/243,693
19 <151> PRIOR FILING DATE: 2000-10-27
21 <160> NUMBER OF SEQ ID NOS: 2
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 829
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
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33 Cys Trp Leu Gln Cys Ala Ala Ser Glu Pro Cys Arg Ala Val Phe Arg
34              20                  25                  30
35 Glu Ala Glu Val Thr Leu Glu Ala Gly Gly Ala Glu Gln Glu Pro Gly
36              35                  40                  45
37 Gln Ala Leu Gly Lys Val Phe Met Gly Cys Pro Gly Gln Glu Pro Ala
38      50                  55                  60
39 Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg Asn Gly Glu Thr
40 65                  70                  75                  80
41 Val Gln Glu Arg Arg Ser Leu Lys Glu Arg Asn Pro Leu Lys Ile Phe
42              85                  90                  95
43 Pro Ser Lys Arg Ile Leu Arg Arg His Lys Arg Asp Trp Val Val Ala
44             100                 105                 110
45 Pro Ile Ser Val Pro Glu Asn Gly Lys Gly Pro Phe Pro Gln Arg Leu
46         115                 120                 125
47 Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr Lys Ile Phe Tyr Ser
48      130                 135                 140
49 Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu Gly Val Phe Ala Val
50 145                 150                 155                 160
51 Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys Pro Leu Asp Arg Glu
52              165                 170                 175
53 Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala Val Ser Glu Asn Gly
54              180                 185                 190
55 Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile Ile Val Thr Asp Gln
```

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56          195                 200                 205
57 Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr Phe Arg Gly Ser Val
58     210                 215                 220
59 Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met Gln Val Thr Ala Thr
60 225                 230                 235                 240
61 Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly Val Val Ala Tyr Ser
62                 245                 250                 255
63 Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile
64             260                 265                 270
65 His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg
66         275                 280                 285
67 Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln Ala Thr Asp Met Asp
68     290                 295                 300
69 Gly Asp Gly Ser Thr Thr Thr Ala Val Ala Val Val Glu Ile Leu Asp
70 305                 310                 315                 320
71 Ala Asn Asp Asn Ala Pro Met Phe Asp Pro Gln Lys Tyr Glu Ala His
72                 325                 330                 335
73 Val Pro Glu Asn Ala Val Gly His Glu Val Gln Arg Leu Thr Val Thr
74             340                 345                 350
75 Asp Leu Asp Ala Pro Asn Ser Pro Ala Trp Arg Ala Thr Tyr Leu Ile
76         355                 360                 365
77 Met Gly Gly Asp Asp Gly Asp His Phe Thr Ile Thr Thr His Pro Glu
78     370                 375                 380
79 Ser Asn Gln Gly Ile Leu Thr Thr Arg Lys Gly Leu Asp Phe Glu Ala
80 385                 390                 395                 400
81 Lys Asn Gln His Thr Leu Tyr Val Glu Val Thr Asn Glu Ala Pro Phe
82             405                 410                 415
83 Val Leu Lys Leu Pro Thr Ser Thr Ala Thr Ile Val Val His Val Glu
84         420                 425                 430
85 Asp Val Asn Glu Ala Pro Val Phe Val Pro Pro Ser Lys Val Val Glu
86         435                 440                 445
87 Val Gln Glu Gly Ile Pro Thr Gly Glu Pro Val Cys Val Tyr Thr Ala
88     450                 455                 460
89 Glu Asp Pro Asp Lys Glu Asn Gln Lys Ile Ser Tyr Arg Ile Leu Arg
90 465                 470                 475                 480
91 Asp Pro Ala Gly Trp Leu Ala Met Asp Pro Asp Ser Gly Gln Val Thr
92             485                 490                 495
93 Ala Val Gly Thr Leu Asp Arg Glu Asp Glu Gln Phe Val Arg Asn Asn
94         500                 505                 510
95 Ile Tyr Glu Val Met Val Leu Ala Met Asp Asn Gly Ser Pro Pro Thr
96         515                 520                 525
97 Thr Gly Thr Gly Thr Leu Leu Leu Thr Leu Ile Asp Val Asn Asp His
98     530                 535                 540
99 Gly Pro Val Pro Glu Pro Arg Gln Ile Thr Ile Cys Asn Gln Ser Pro
100 545                 550                 555                 560
101 Val Arg His Val Leu Asn Ile Thr Asp Lys Asp Leu Ser Pro His Thr
102             565                 570                 575
103 Ser Pro Phe Gln Ala Gln Leu Thr Asp Asp Ser Asp Ile Tyr Trp Thr
104         580                 585                 590
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105 Ala Glu Val Asn Glu Glu Gly Asp Thr Val Val Leu Ser Leu Lys Lys
106         595             600             605
107 Phe Leu Lys Gln Asp Thr Tyr Asp Val His Leu Ser Leu Ser Asp His
108     610             615             620
109 Gly Asn Lys Glu Gln Leu Thr Val Ile Arg Ala Thr Val Cys Asp Cys
110 625             630             635             640
111 His Gly His Val Glu Thr Cys Pro Gly Pro Trp Lys Gly Gly Phe Ile
112             645             650             655
113 Leu Pro Val Leu Gly Ala Val Leu Ala Leu Leu Phe Leu Leu Leu Val
114         660             665             670
115 Leu Leu Leu Leu Val Arg Lys Lys Arg Lys Ile Lys Glu Pro Leu Leu
116         675             680             685
117 Leu Pro Glu Asp Asp Thr Arg Asp Asn Val Phe Tyr Tyr Gly Glu Glu
118     690             695             700
119 Gly Gly Gly Glu Glu Asp Gln Asp Tyr Asp Ile Thr Gln Leu His Arg
120 705             710             715             720
121 Gly Leu Glu Ala Arg Pro Glu Val Val Leu Arg Asn Asp Val Ala Pro
122             725             730             735
123 Thr Ile Ile Pro Thr Pro Met Tyr Arg Pro Arg Pro Ala Asn Pro Asp
124             740             745             750
125 Glu Ile Gly Asn Phe Ile Ile Glu Asn Leu Lys Ala Ala Asn Thr Asp
126         755             760             765
127 Pro Thr Ala Pro Pro Tyr Asp Thr Leu Leu Val Phe Asp Tyr Glu Gly
128     770             775             780
129 Ser Gly Ser Asp Ala Ala Ser Leu Ser Ser Leu Thr Ser Ser Ala Ser
130 785             790             795             800
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133 Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu Asp Asp
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138 <211> LENGTH: 3170
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145 cctccgagcc gtgccgggcg gtcttcaggg aggctgaagt gaccttggag gcgggaggcg 180
146 cggagcagga gcccggccag gcgctgggga aagtattcat gggctgccct gggcaagagc 240
147 cagctctgtt tagcactgat aatgatgact tcactgtgcg gaatggcgag acagtccagg 300
148 aaagaaggtc actgaaggaa aggaatccat tgaagatctt cccatccaaa cgtatcttac 360
149 gaagacacaa gagagattgg gtggttgctc caatatctgt ccctgaaaat ggcaagggtc 420
150 ccttccccca gagactgaat cagctcaagt ctaataaaga tagagacacc aagattttct 480
151 acagcatcac ggggccgggg gcagacagcc cccctgaggg tgtcttcgct gtagagaagg 540
152 agacaggctg gttgttgttg aataagccac tggaccggga ggagattgcc aagtatgagc 600
153 tctttggcca cgctgtgtca gagaatggtg cctcagtgga ggaccccatg aacatctcca 660
154 tcatcgtgac cgaccagaat gaccacaagc ccaagtttac ccaggacacc ttccgaggga 720
155 gtgtcttaga gggagtccta ccaggtactt ctgtgatgca ggtgacagcc acagatgagg 780
156 atgatgccat ctacacctac aatggggtgg ttgcttactc catccatagc caagaaccaa 840
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157 aggacccaca cgacctcatg ttcacaattc accggagcac aggcaccatc agcgtcatct 900
158 ccagtggcct ggaccgggaa aaagtccctg agtacacact gaccatccag gccacagaca 960
159 tggatgggga cggctccacc accacggcag tggcagtagt ggagatcctt gatgccaatg 1020
160 acaatgctcc catgtttgac ccccagaagt acgaggccca tgtgcctgag aatgcagtgg 1080
161 gccatgaggt gcagaggctg acggtcactg atctggacgc ccccaactca ccagcgtggc 1140
162 gtgccaccta ccttatcatg ggcggtgacg acggggacca ttttaccatc accacccacc 1200
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168 cagggtggct agccatggac ccagacagtg ggcaggtcac agctgtgggc accctcgacc 1560
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194 atactgagtg tgcctaggtt gccccttatt ttttattttc cctgttgcgt tgctatagat 3120
195 aagggtgagg acaatcgtgt atatgtacta gaactttttt attaaagaaa         3170
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